

D. GORD

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1636

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/145,916

DATE: 07/18/2000  
TIME: 13:58:11

Input Set : A:\Bis-039  
Output Set: N:\CRF3\07182000\I145916.raw

SEQUENCE LISTING

1 (1) GENERAL INFORMATION:

- 2 (i) APPLICANT: Simons, Michael  
3 Volk, Rudiger  
4 Horowitz, Arie  
5 (ii) TITLE OF INVENTION: Stimulation of angiogenesis  
6 via enhanced endothelial expression of syndecan-4  
7 core proteins  
8 (iii) NUMBER OF SEQUENCES: 16  
9 (iv) CORRESPONDENCE ADDRESS:  
10 (A) ADDRESSEE: David Prashker, Esq.  
11 (B) STREET: P.O. Box 5387  
12 (C) CITY: Magnolia  
13 (D) STATE: Massachusetts  
14 (E) COUNTRY: USA  
15 (F) ZIP: 01930  
16 (v) COMPUTER READABLE FORM:  
17 (A) MEDIUM TYPE: Diskette, 3.50 inch, 1.40 Mb storage  
18 (B) COMPUTER: IBM PS/1  
19 (C) OPERATING SYSTEM: MS DOS  
20 (D) SOFTWARE: WordPerfect version 5.1

C--> 21 (vi) CURRENT APPLICATION DATA:

- C--> 22 (A) APPLICATION NUMBER: US/09/145,916  
C--> 23 (B) FILING DATE: 02-Sep-1998  
24 (C) CLASSIFICATION: Unknown

25 (viii) ATTORNEY/AGENT INFORMATION:

- 26 (A) NAME: David Prashker, Esq.  
27 (B) REGISTRATION NUMBER: 29,693  
28 (C) REFERENCE/DOCKET NUMBER: BIS-039  
29 (ix) TELECOMMUNICATION INFORMATION:  
30 (A) TELEPHONE: (978) 525-3794

31 (2) INFORMATION FOR SEQ ID NO: 1:

32 (i) SEQUENCE CHARACTERISTICS:

- 33 (A) LENGTH: 762 base pairs  
34 (B) TYPE: nucleic acid  
35 (C) STRANDEDNESS: single  
36 (D) TOPOLOGY: linear

37 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

39 ATGAGACGTG CGGCGCTCTG GCTTTGGCTC TGC GCGCTGG CGCTGCGCCT GCAGCCTGCC 60  
40 CTCCCGCAAA TTGTCACCGC AAATGTGCCT CCTGAAGACC AAGATGGCTC TGGGGACGAC 120  
41 TCAGACAACT TCTCTGGCTC AGGCACAGGT GCTTTGCCAG ATATGACTTT GTCACGGCAG 180  
42 ACACCTTCCA CTTGGAAGGA TGTGTGGCTC CTGACAGCTA CACCCACAGC TCCAGAACCC 240  
43 ACCAGCAGGG ATACCGAGGC CACCCTCACC TCTATCCTGC CGGCTGGAGA GAAGCCTGAG 300  
44 GAGGGAGAGC CCGTGGCCCA CGTGAAGCA GAGCCTGACT TCACTGCTCG GGACAAGGAG 360  
45 AAGGAGGCCA CCACCAGGCC TAGGGAGACC ACACAGCTCC CAGTCACCCA ACAGGCCTCA 420  
46 ACAGCAGCCA GAGCCACCAC GGCCCAGGCA TCTGTCACGT CTCATCCCCA CGGGGATGTG 480  
47 CAACCTGGCC TCCACGAGAC CTTGGCTCCC ACAGCACCCG GCCAACCTGA CCATCAGCCT 540

ENTERED

RECEIVED

AUG 02 2000

TECH CENTER 1600/2900

87	Gly	Arg	Arg	Glu	Gly	Ala	Arg	Gly	Lys	Glu	Glu	Glu	Glu	Lys	Glu	Glu
88	1				5					10					15	
89	Asp	Pro	Gly	Arg	Glu	Ala	Arg	Arg	Gly	Arg	Arg	Arg	Gly	Ala	Ala	Ala
90				20					25					30		
91	Glu	Pro	Val	Ala	Pro	Leu	Gly	Arg	Ala	Ala	Leu	Gln	Ile	Pro	Pro	Glu
92			35					40					45			
93	Leu	Gln	Pro	Arg	Gly	Ser	Arg	Ala	Pro	Ala	Ala	Leu	Pro	Leu	Asn	Phe
94		50					55					60				
95	Cys	Arg	Ser	Ser	Leu	Ser	Gln	Arg	Ile	Tyr	Ser	Leu	Lys	Pro	Glu	
96	65					70				75					80	
97	Thr	Glu	Pro	Arg	His	Gly	Lys	Gly	Val	Arg	Gly	Gly	Ala	Lys	Pro	Gln
98					85					90					95	
99	Gln	Ser	Lys	Lys	Ser	Phe	Arg	Glu	Gln	Pro	Ser	Arg	Ser	Thr	Asn	Ser
100				100					105					110		

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101 Val Ser Gly Val Gln Lys Pro Thr Ser Glu Arg Ala Pro Arg Ser Arg
102      115      120      125
103 Gly Ala Ala Ala Gly Gly Gly Ser Arg Arg Arg Arg Arg Lys Arg Ala
104      130      135      140
105 Pro Pro Ser Pro Glu Pro Glu Ser Pro Ser Leu Ser Arg Asn Arg Cys
106 145      150      155      160
107 Gly Thr Leu Leu Arg Ile Arg Val Arg Gly Leu Ala Glu Arg Trp Ala
108      165      170      175
109 Gly Gly Phe Val Leu Pro Trp Leu Gln Ala Ala Ala Gly Ser Ser Arg
110      180      185      190
111 Ser Leu Gly Asn Met Arg Arg Ala Trp Ile Leu Leu Thr Leu Gly Leu
112      195      200      205
113 Val Ala Cys Val Ser Ala Glu Ser Arg Ala Glu Leu Thr Ser Asp Lys
114      210      215      220
115 Asp Met Tyr Leu Asp Asn Ser Ser Ile Glu Glu Ala Ser Gly Val Tyr
116 225      230      235      240
117 Pro Ile Asp Asp Asp Tyr Ala Ser Ala Ser Gly Ser Gly Ala Asp
118      245      250      255
119 Glu Asp Val Glu Ser Pro Glu Leu Thr Thr Thr Arg Pro Leu Pro Lys
120      260      265      270
121 Ile Leu Leu Thr Ser Ala Ala Pro Lys Val Glu Thr Thr Thr Leu Asn
122      275      280      285
123 Ile Gln Asn Lys Ile Pro Ala Gln Thr Lys Ser Pro Glu Glu Thr Asp
124      290      295      300
125 Lys Glu Lys Val His Leu Ser Asp Ser Glu Arg Lys Met Asp Pro Ala
126 305      310      315      320
127 Glu Glu Asp Thr Asn Val Tyr Thr Glu Lys His Ser Asp Ser Leu Phe
128      325      330      335
129 Lys Arg Thr Glu
130      340

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132 (2) INFORMATION FOR SEQ ID NO: 4:

133 (i) SEQUENCE CHARACTERISTICS:

134 (A) LENGTH: 1079 base pairs

135 (B) TYPE: nucleic acid

136 (C) STRANDEDNESS: single

137 (D) TOPOLOGY: linear

138 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

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140 GCGGCGGCGC GCTGCTGAGC CGTCCTTGCG GCACGSSGAT GCGGCGGAG CTGCGGCGCC 60
141 TCGCGGTGCT GCTGCTGCTG CTCAGCGCCC GCGCAGCGCT GGCTCAGCCG TGGCGCAATG 120
142 AGAACTACGA GAGGCCGGTG GACCTGGAGG GCTCTGGGGA TGATGATCCC TTTGGGGACG 180
143 ATGAACTGGA TGACATCTAC TCGGGCTCCG GCTCAGGCTA TTTTGAGCAG GAGTCAGGGT 240
144 TGGAGACAGC GGTGAGCCTC ACCACGGACA CGTCCGTCCC ACTGCCCACC ACGGTGGCCG 300
145 TGCTGCCTGT CACCTTGGTG CAGCCCATGG CAACACCCTT TGAGCTGTTC CCCACAGAGG 360
146 ACACGTCCCC TGAGCAAACA ACCAGCGTCT TGTATATCCC CAAGATAACA GAAGCACCAG 420
147 TGATCCCCAG CTGGAAAACA ACCACCGCCA GTACCACTGC CAGTGACTCC CCCAGTACCA 480
148 CCTCCACCAC CACCACCACG GCTGCTACCA CCACCACAAC CACCACCACC ATCAGCACCA 540
149 CTGTGGCCAC CTCCAAGCCC ACCACTACCC AGAGGTTCTT GCGGCTTTT GTCACCAAGG 600
150 CAGCCACCAC CCGGGCCACC ACCCTGGAGA CGCCACCAC CTCCATCCCT GAAACCAAGT 660
151 TCCTGACAGA GGTGACCACA TCACGGCTTG TCCCTCCAG CACAGCCAAG CCGAGGTCCC 720

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152 TGCCAAAACC AAGCACTTCC AGGACTGCAG AACCCACGGA AAAAAGCACT GCCTTGCCCTT 780
153 CCAGCCCCAC CACGCTGCCA CCCACAGAAG CCCCCCAGGT GGAGCCAGGG GAGTTGACGA 840
154 CAGTCCCTCGA CAGTGACCTG GAAGTCCCAA CCAGTAGTGG CCCCAGCGGG GACTTCGAGA 900
155 TCCAGGAGGA GGAGGAGACA ACTCGTCCTG AGCTGGGCAA TGAGGTGGTG GCAGTGGTGA 960
156 CACCACCAGC AGCACCAGGG CTGGGCAAGA ATGCAGAGCC GGGGCTCATC GACAACACAA 1020
157 TAGAGTCGGG CAGCTCGGCT GCTCAGCTCC CCCAGAAAAA CATCCTGGAG AGGAAGGAA 1079
159 (2) INFORMATION FOR SEQ ID NO: 5:
160 (i) SEQUENCE CHARACTERISTICS:
161 (A) LENGTH: 447 base pairs
162 (B) TYPE: nucleic acid
163 (C) STRANDEDNESS: single
164 (D) TOPOLOGY: linear
165 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
167 ATGGCGCCTG TCTGCCTGTT TGCGCCGCTG CTGCTGTTGC TCCTCGGAGG TTTCCCCGTC 60
168 GCCCCAGGCG AGTCGATTCT AGAGACTGAG GTCATAGACC CCCAGGACCT CCTGGAAGGC 120
169 AGATACTTCT CTGGAGCCCT CCCGGACGAT GAAGACGCTG GGGGCCCTGA GCAGGACTCT 180
170 GACTTTGAGC TGTCGGGTTC CGGAGATCTA GATGACACGG AGGAGCCCAG GACCTTCCCT 240
171 GAGGTGATTT CACCCTTGGT GCCACTAGAT AACCACATCC CCGAGAATGC CCAGCCTGGC 300
172 ATCCGTGTCC CCTCAGAGCC CAAGGAAGTG GAAGAGAATG AGGTCATTCC CAAAAGGGTC 360
173 CCCTCCGACG TGGGGGATGA CGATGTGTCC AACAAAGTGT CCATGTCCAG CACTTCCCAG 420
174 GGCAGCAACA TTTTGAAG AACTGAG 447
176 (2) INFORMATION FOR SEQ ID NO: 6:
177 (i) SEQUENCE CHARACTERISTICS:
178 (A) LENGTH: 1590 base pairs
179 (B) TYPE: nucleic acid
180 (C) STRANDEDNESS: single
181 (D) TOPOLOGY: linear
182 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
184 ATGGAGCTCC GGGCCCGAGG CTGGTGGCTG CTGTGCGCGG CCGCCGCGCT AGTCGCCTGC 60
185 GCCCCGCGGG ACCCCGCCAG CAAGAGCCGG AGCTGCAGCG AAGTCCGCCA GATCTACGGG 120
186 GCTAAGGGCT TTAGCCTGAG CGACGTGCCC CAGGCAGAGA TCTCGGGAGA GCACCTGCGG 180
187 ATCTGCCCCC AGGGCTACAC CTGCTGCACC AGTGAGATGG AGGAGAACCT GGCCAACCAC 240
188 AGCCGGATGG AGCTGGAGAC CGCACTCCAC GACAGCAGCC GTGCCCTGCA GGCTACACTG 300
189 GCCACCCAGC TGCATGGCAT CGATGACCAC TTCCAGCGCC TGCTGAATGA CTCGGAGCGT 360
190 AACTGTCAGG ATGCTTTTCC CGGGGCCCTT GGGGACCTGT ACACGCAGAA CACTCGGGCC 420
191 TTCCGGGACC TGTATGCTGA GCTGCGTCTC TACTACCGAG GGGCCAACCT ACACCTTGAG 480
192 GAGACACTGG CCGAGTTCTG GGCACGGCTG CTGGAGCGTC TCTTCAAGCA GCTGCACCCC 540
193 CAGCTTCTGC TGCCCGATGA CTATCTGGAC TGCCTGGGCA AGCAGGCAGA GGCCTGCGG 600
194 CCGTTTGGGG ATGCCCCCTG AGAACTGCGC CTGAGGGCCA CCCGTGCTTT TGTGGCGGCA 660
195 CGATCCTTTG TGCAGGGCCT GGGTGTGGCC AGTGACGTAG TCCGAAAGGT GGCCAGGTT 720
196 CCTCTGGCCC CAGAATGTTT TCGGGCTGTC ATGAAGTTGG TCTACTGTGC CCATTGCCGG 780
197 GGAGTCCCTG GTGCCCCGCC CTGTCCCGAC TATTGCCGAA ATGTGCTCAA AGGCTGCCTT 840
198 GCCAACCAGG CCGACCTGGA TGCCGAGTGG AGGAACCTCC TGGACTCCAT GGTGCTCATC 900
199 ACTGACAAGT TCTGGGGCCC GTCGGGTGCG GAGAATGTCA TTGGCAGTGT GCATATGTGG 960
200 CTGGCGGAGG CCATCAACGC CCTCCAGGAC AACAAGGACA CACTCACAGC TAAGGTCATC 1020
201 CAGGGCTGCG GAAACCCCAA GGTCAATCCC CATGGCTCTG GGCCTGAGGA GAAGCGTCGC 1080
202 CGTGGCAAAC TGGCACTGCA GGAGAAGTCC TCCACAGGTA CTCTGGAATA GCTGGTCTCT 1140
203 GAGGCCAAGG CCCAGCTCCG AGACATTGAG GACTACTGGA TCAGCCTCCC AGGGACACTG 1200
204 TGTAGTGAGA AGATGGCCAT GAGTCCTGCC AGCGATGACC GCTGCTGGAA TGGGATTTCC 1260

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205 AAGGGCCGGT ACCTACCTGA GGTGATGGGT GATGGGCTGG CCAACCAGAT CAACAACCCT 1320  
 206 GAAGTGGAGG TGGACATCAC CAAGCCGGAT ATGACCATCC GGCAGCAGAT CATGCAGCTC 1380  
 207 AAGATCATGA CCAACCGTTT ACGTGGCGCC TACGGTGGCA ATGATGTGGA CTTCCAGGAT 1440  
 208 GCCAGTGATG ACGGCAGTGG CTCCGGCAGC GGTGGCGGAT GCCCAGATGA CGCCTGTGGC 1500  
 209 CGGAGGGTCA GCAAGAAGAG CTCCAGCTCC CGGACCCCTT TGACCCATGC CCTCCCCGGC 1560  
 210 TTGTCAGAAC AGGAGGGACA GAAGACCTCG 1590

212 (2) INFORMATION FOR SEQ ID NO: 7:

213 (i) SEQUENCE CHARACTERISTICS:

214 (A) LENGTH: 531 amino acids

215 (B) TYPE: amino acid

216 (C) STRANDEDNESS: single

217 (D) TOPOLOGY: linear

218 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

220 Met Glu Leu Arg Ala Arg Gly Trp Trp Leu Leu Cys Ala Ala Ala Ala  
 221 1 5 10 15  
 222 Leu Val Ala Cys Ala Arg Gly Asp Pro Ala Ser Lys Ser Arg Ser Cys  
 223 20 25 30  
 224 Ser Glu Val Arg Gln Ile Tyr Gly Ala Lys Gly Phe Ser Leu Ser Asp  
 225 35 40 45  
 226 Val Pro Gln Ala Glu Ile Ser Gly Glu His Leu Arg Ile Cys Pro Gln  
 227 50 55 60  
 228 Gly Tyr Thr Cys Cys Thr Ser Glu Met Glu Glu Asn Leu Ala Asn His  
 229 65 70 75 80  
 230 Ser Arg Met Glu Leu Glu Thr Ala Leu His Asp Ser Ser Arg Ala Leu  
 231 85 90 95  
 232 Gln Ala Thr Leu Ala Thr Gln Leu His Gly Ile Asp Asp His Phe Gln  
 233 100 105 110  
 234 Arg Leu Leu Asn Asp Ser Glu Arg Thr Leu Gln Asp Ala Phe Pro Gly  
 235 115 120 125  
 236 Ala Phe Gly Asp Leu Tyr Thr Gln Asn Thr Arg Ala Phe Arg Asp Leu  
 237 130 135 140  
 238 Tyr Ala Glu Leu Arg Leu Tyr Tyr Arg Gly Ala Asn Leu His Leu Glu  
 239 145 150 155 160  
 240 Glu Thr Leu Ala Glu Phe Trp Ala Arg Leu Leu Glu Arg Leu Phe Lys  
 241 165 170 175  
 242 Gln Leu His Pro Gln Leu Leu Leu Pro Asp Asp Tyr Leu Asp Cys Leu  
 243 180 185 190  
 244 Gly Lys Gln Ala Glu Ala Leu Arg Pro Phe Gly Asp Ala Pro Arg Glu  
 245 195 200 205  
 246 Leu Arg Leu Arg Ala Thr Arg Ala Phe Val Ala Ala Arg Ser Phe Val  
 247 210 215 220  
 248 Gln Gly Leu Gly Val Ala Ser Asp Val Val Arg Lys Val Ala Gln Val  
 249 225 230 235 240  
 250 Pro Leu Ala Pro Glu Cys Ser Arg Ala Val Met Lys Leu Val Tyr Cys  
 251 245 250 255  
 252 Ala His Cys Arg Gly Val Pro Gly Ala Arg Pro Cys Pro Asp Tyr Cys  
 253 260 265 270  
 254 Arg Asn Val Leu Lys Gly Cys Leu Ala Asn Gln Ala Asp Leu Asp Ala  
 255 275 280 285

VERIFICATION SUMMARY                      DATE: 07/18/2000  
PATENT APPLICATION:    US/09/145,916              TIME: 13:58:12

Input Set : A:\Bis-039  
Output Set: N:\CRF3\07182000\I145916.raw

L:21 M:220 C: Keyword misspelled or invalid format, [(vi) CURRENT APPLICATION DATA:]  
L:22 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]  
L:23 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]